Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method of ~~amplification of~~ amplifying RNA in a nucleic acid sample to obtain sense strand cDNA fragments from said RNA, comprising:

(a) obtaining a nucleic acid sample comprising RNA;

(b) contacting the nucleic acid sample with the appropriate reagents to synthesize a first strand cDNA using the RNA as template;

(c) synthesizing a second strand cDNA comprising UTP, using said first strand cDNA as template in a reaction mixture comprising dUTP;

(d) nicking the second strand cDNA at one or more positions where dUTP was incorporated to generate one or more nicks; and

(e) extending the second strand cDNA from the one or more nicks in a reaction mixture comprising dUTP and a DNA polymerase with strand displacing activity, wherein downstream fragments of the second strand cDNA are displaced to obtain sense strand cDNA fragments from said RNA.

2. (original) The method of claim 1 wherein steps (d) and (e) are performed simultaneously in a single reaction.

3. (original) The method of claim 1 wherein step (d) comprises: generating abasic sites in the second strand cDNA and cleaving the second strand cDNA at the abasic sites.

4. (original) The method of claim 3 wherein the abasic sites are generated by incubating with a uracil DNA glycosylase enzyme.

5. (original) The method of claim 3 wherein the step of cleaving the second strand cDNA at the abasic sites comprises incubating the second strand cDNA with an apurinic endonuclease.

6. (original) The method of claim 5 wherein the apurinic endonuclease is Endonuclease IV

7. (original) The method of claim 3 wherein the step of cleaving the second strand cDNA at abasic sites comprises incubating the second strand cDNA at high temperature.

8. (original) The method of claim 3 wherein the step of cleaving the second strand cDNA at abasic sites comprises incubating the second strand cDNA under alkaline conditions.

9. (original) The method of claim 1 wherein first strand cDNA is synthesized in the presence of an RNA dependent DNA polymerase and second strand cDNA is synthesized in the presence of a DNA dependent DNA polymerase.

10. (original) The method of claim 1 wherein the strand displacing DNA polymerase is selected from the group consisting of the Klenow fragment, Bst and phi29.

11. (original) The method of claim 1 wherein the DNA polymerase is a phi29 variant that has reduced exonuclease activity.

12. (original) The method of claim 1 wherein steps (d) and (e) are performed under isothermal conditions.

13. (original) The method of claim 1 wherein steps (d) and (e) are performed at 37C.

14. (original) The method of claim 1 wherein Endonuclease V is used to nick the second strand cDNA in step (d).

15. (original) The method of claim 1 wherein the reaction mixture of step (c) further comprises dTTP and the ratio of dTTP to dUTP in the starting mixture is greater than about 5 to 1.

16. (original) The method of claim 1 the reaction mixture of step (e) further comprises a labeled nucleotide.

17. (original) The method of claim 16 wherein the labeled nucleotide is biotin-dATP.

18. (original) The method of claim 1 wherein the first strand cDNA is synthesized by a method comprising: hybridizing at least one primer to the nucleic acid sample and extending the primer with a polymerase.

19. (original) The method of claim 18 wherein the nucleic acid sample comprises RNA and the polymerase is an RNA dependent DNA polymerase.

20. (original) The method of claim 18 wherein the at least one primer comprises a 3' oligo dT portion.

21. (original) The method of claim 18 wherein the at least one primer comprises a mixture of primers of random sequence wherein the primers are of a common length and the length is between 6 and 15 nucleotides.

22. (currently amended) A method of detecting a target sequence in a nucleic acid sample comprising RNA, said method ~~a complex mixture of sequences~~ comprising:
(a) amplifying the nucleic acid sample by the method of claim 1;
(b) labeling the nucleic acids in the amplified nucleic acid sample with a detectable label;
(c) hybridizing the labeled, amplified nucleic acids to an array of probes comprising at least one probe that is perfectly complementary to the target sequence over the length of the probe;
(d) detecting a hybridization pattern; and,

(e) determining if the target sequence is present or absent based on the hybridization pattern.

23. (original) The method of claim 21 wherein the label is biotin.

24. (currently amended) The method of claim 1 wherein ~~the nucleic acid sample comprises RNA and~~ first strand cDNA is synthesized using an RNA dependent DNA polymerase.

25. (original) The method of claim 20 wherein first strand cDNA is synthesized by a primer comprising oligo dT.

26. (original) The method of claim 20 wherein first strand cDNA synthesis is primed by a plurality of locus specific primers.

27. (original) The method of claim 1 wherein the nucleic acid comprises genomic DNA.

28. (original) The method of claim 23 wherein first strand cDNA synthesis is primed by a plurality of locus specific primers.

29. (original) The method of claim 1 wherein the nucleic acid sample comprises adaptor ligated DNA fragments.

30. (original) The method of claim 1 wherein the nucleic acid sample comprises adaptor ligated DNA fragments that have been amplified by PCR.

Claims 31-37. (canceled)